

Serial No.: 10/552,857

Response to Office Action mailed: February 18, 2010

Amendment Dated: August 18, 2010

#### REMARKS/ARGUMENTS

This is in response to the Office Action mailed February 18, 2010 for the above-captioned application. An extension of time sufficient to make this paper timely is requested and the appropriate fee is enclosed.

Claims 62-64 and 74 have been canceled without prejudice or disclaimer. Claims 65-71, 73, 75, and 76 are amended. Claims 77-82 are added. No new matter has been added. Therefore, claims 65-73 and 75-82 are now pending. Claims 65, 69, 71, 75, and 77 are independent claims.

Claims 62-76 stand rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the written description requirement. Of these claims, claims 65-73, 75, and 76 remain pending. Based on the Examiner's statement of the claim interpretation to support the claim rejection, Applicants believe that the amendments made herein fully address the rejection as directed to the claims.

With respect to claims 65-68, the Office alleges that "[t]he structural features that distinguish those nucleic acids that modify the levels of chalcone synthase, dihydroflavonol 4-reductase and leucoanthocyanidine reductase in a plant cell from those that do not are not described in the specification." Applicants respectfully disagree, as these structural features are shown in the sequences and plasmid maps disclosed. Further, pages 5 and 6 of the originally filed Specification discuss conservative amino acid substitutions. *See* Specification at paragraphs [0022] and [0023]. For the Examiner's convenience, nucleotide and amino acid alignments of TrCHS3a, TrCHSc, TrCHSf and TrCHSh, as well as TrLARA, TrLARb and TrLARc, identifying conserved regions are included as Appendix A.

Claims 62-76 also stand rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention. In view of the amendments made herein, Applicants respectfully request reconsideration and withdrawal of this rejection.

With respect to the recitation of "dihydroflavonol 4-reductase (BAN)," Applicants respectfully submit that, at the time the present application was filed, BAN was thought to be DFR-like, hence the nomenclature used in the patent application. BAN is now thought to be a member of the ANR family of genes. BAN is the nomenclature given to the flavonoid biosynthetic gene, *Banyuls*, in *Arabidopsis thaliana*, but it is used somewhat loosely in the literature. Anthocyanidin reductase (*ANR*) is the name now given to the homolog of BAN in *Trifolium repens* (*TrANR*). *TrLAR* (Leucoanthocyanidin 4 reductase) is another very closely related *T. repens* gene. ANR is a more generic term.

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Claims 65 and 67 stand rejected under 35 U.S.C. § 102 as being anticipated by Suzuki et al. (2000, Mol. Breed. 6:239-246). The Examiner stated that the basis for this rejection was that the sequences disclosed by Suzuki would have a at least a portion that is 90% identity to “the relevant part” of 2, 4, 6, or 8 and at least 90% identity to the “relevant part” of SEQ ID NO: 10, and are at least 60 nucleotides long. However, this rejection is based on the construction of the fragment length as being as few as two bases. The amendment of Claims 65 and 67 is believed to overcome this rejection.

Claims 62-76 stand rejected under 35 U.S.C. § 103 (a) as being unpatentable over Spangenberg et al. (U.S. Patent Application Publication No. 2005/0069884). However, Spangenberg is disqualified as prior art under 35 U.S.C. § 103(c). 35 U.S.C. § 103(c)(1) states:

Subject matter developed by another person, which qualifies as prior art only under one or more of subsections (e), (f) and (g) of section 102 of this title, shall not preclude patentability under this section where the subject matter and the claimed invention were, at the time the claimed invention was made, owned by the same person or subject to an obligation of assignment to the same person.

For the purposes of 35 U.S.C. § 103(c), a “person” may be a corporation. Spangenberg et al. could qualify as a prior art reference only under 35 U.S.C. § 102(e), and both Spangenberg et al. and the present pending application were under an obligation of assignment to Agriculture Victoria Services Pty Ltd. and Agresearch Limited at the time the claimed invention was made. Thus, Spangenberg et al. does not qualify as prior art per 35 U.S.C. §103(c). Accordingly, this rejection is improper and must be withdrawn.

Claims 62-76 stand rejected under 35 U.S.C. § 103(a) as being unpatentable over Dixon et al. (U.S. Patent Application Publication No. 2004/0093632) in view of Arioli et al. (1994, Gene 138:79-86. Dixon et al. describes plants transformed with a LAR (which Dixon et al. calls a BAN gene) and mentions in paragraph [0062] the possibility of a DFR/LAR combination. The Examiner also alleges that the Dixon et al. at paragraph [0010] teaches a combination of chalcone synthase with LAR. However, Dixon et al. refers to chalcone isomerase, rather than chalcone synthase. Chalcone isomerase is a different enzyme from chalcone synthase, and has different specific activity acting on a different substrate. For at least these reasons, the combination of Dixon et al. and Arioli et al. fails to obviate claims 65-76, or newly added claims 77-82.

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In view of the foregoing, Applicants submit that all of the claims of this application are now in form for allowance, and such action is respectfully urged.

Respectfully submitted,

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## APPENDIX A

### TrCHS nucleotide sequence alignment

TrCHS3as : GAATTC<sup>1</sup>ACTAGT<sup>2</sup>GATTAAGCAGTGGTAACAACGCAGAGTACGCGGG<sup>3</sup>GAA<sup>4</sup>-----CAA<sup>5</sup>AAA<sup>6</sup> :  
55  
TrCHS3cs : GAATTC<sup>1</sup>-----GATTAAGCAGTGGTAACAACGCAGAGTACGCGGG<sup>2</sup>CATT<sup>3</sup>-----CAATCT<sup>4</sup> :  
50  
TrCHS3fs : GAATTC<sup>1</sup>-----GATTAAGCAGTGGTAACAACGCAGAGTACGCGGG<sup>2</sup>ACT<sup>3</sup>-----AAG<sup>4</sup>CC<sup>5</sup> :  
48  
TrCHS3shs : GAATTC<sup>1</sup>ACTAGT<sup>2</sup>GATTAAGCAGTGGTAACAACGCAGAGTACGCGGG<sup>3</sup>GAAATCCA<sup>4</sup>CCAAT<sup>5</sup> :  
60

TrCHS3as : CAACT<sup>1</sup>ACG<sup>2</sup>-----CATATTATAT<sup>3</sup>ATATAT<sup>4</sup>-----ATATATAGTCTATATAATTGAA<sup>5</sup> :  
99  
TrCHS3cs : GTTC<sup>1</sup>GCAT<sup>2</sup>-----AAAATTCACT<sup>3</sup>CATTGCATAGAAAACCATACACATT<sup>4</sup>TGATCTTGC<sup>5</sup>AAAGAA<sup>6</sup> :  
109  
TrCHS3fs : TTGA<sup>1</sup>TCAT<sup>2</sup>-----TGT<sup>3</sup>TGTTTCCATAACACA<sup>4</sup>-----AGAACTAGTGT<sup>5</sup>TTGCT<sup>6</sup>TIGAA<sup>7</sup> :  
96  
TrCHS3shs : CAACAC<sup>1</sup>CATTAAATAACCTTC<sup>2</sup>CAAAT<sup>3</sup>TCTCGTTACCTCACCAAAT<sup>4</sup>CTCATTTTTCAT<sup>5</sup>ATA<sup>6</sup> :  
120

TrCHS3as : AGAAACT<sup>1</sup>CTAAAAGATA<sup>2</sup>TA<sup>3</sup>-----TTA<sup>4</sup>-----ACATAT<sup>5</sup>-----GGTGAGTGTAGCT<sup>6</sup>GAA<sup>7</sup> :  
144  
TrCHS3cs : GAAATAT<sup>1</sup>GGGAGACG<sup>2</sup>-----A<sup>3</sup>-----ACGTAT<sup>4</sup>-----AGTGAGAGGTG<sup>5</sup>----- :  
142  
TrCHS3fs : TCTTAAGAAAA<sup>1</sup>AATGCC<sup>2</sup>TCAAGG<sup>3</sup>TGATT<sup>4</sup>TGAATGGAAGT<sup>5</sup>TCTC<sup>6</sup>GGTGAATGGAGC<sup>7</sup>-----AC<sup>8</sup> :  
154  
TrCHS3shs : TATCT<sup>1</sup>TGGGTACATCTT<sup>2</sup>TG<sup>3</sup>-----TTACCTCCACAAA<sup>4</sup>AAAAAT<sup>5</sup>-----GGTGACCGTAGAAG<sup>6</sup>AG<sup>7</sup> :  
175

TrCHS3as : ATT<sup>1</sup>CGCAAGC<sup>2</sup>CTCAGAGGG<sup>3</sup>CTGA<sup>4</sup>AGGCCCTGCC<sup>5</sup>AACATT<sup>6</sup>TTGGCCAT<sup>7</sup>TGGCACTGCAAAAT<sup>8</sup> :  
204  
TrCHS3cs : -T<sup>1</sup>-CACAAAGC<sup>2</sup>-----AGACAAC<sup>3</sup>CCCTGGGAAGGCTACTATA<sup>4</sup>TTGGCTCT<sup>5</sup>TGGCAAGGCATTC<sup>6</sup> :  
198  
TrCHS3fs : GTGCTAGAC<sup>1</sup>GTG-CTCCTACT<sup>2</sup>TCAGGGAAGGCA<sup>3</sup>AGGATACT<sup>4</sup>TTGCATTAGGAAGGCTTTC<sup>5</sup> :  
213  
TrCHS3shs : ATT<sup>1</sup>CGTAACGCCCAACGTT<sup>2</sup>CAAA<sup>3</sup>TGGGCCCTGCC<sup>4</sup>ACTATCT<sup>5</sup>TAGCTTT<sup>6</sup>TGGCACAGCCACT<sup>7</sup> :  
235

TrCHS3as : CCAC<sup>1</sup>CAAAACCGTGT<sup>2</sup>TGAGCAGAGCACAT<sup>3</sup>-ATCCTGAT<sup>4</sup>TTCTACT<sup>5</sup>TCAAAATTACAAACAG<sup>6</sup> :  
263  
TrCHS3cs : CCTCACC<sup>1</sup>AACTTCTGATGCA<sup>2</sup>-AGAGTGT<sup>3</sup>TTAGTTGATGGTTAT<sup>4</sup>TTTACGGACACTAATTG<sup>5</sup> :  
257  
TrCHS3fs : CCCG<sup>1</sup>CCAGGTCTCCCTCA<sup>2</sup>-AGAGTGT<sup>3</sup>TTGGTGGAAGGATT<sup>4</sup>CAT<sup>5</sup>CCGCACACTAAGTG<sup>6</sup> :  
272  
TrCHS3shs : CCTT<sup>1</sup>CTAACTGTGTCACTCA<sup>2</sup>-AGCTGAT<sup>3</sup>TATCCTGATTACTACT<sup>4</sup>TTTC<sup>5</sup>TATCACCACACAG<sup>6</sup> :  
294

TrCHS3as : TGAGCACAAGACTGAGCT<sup>1</sup>CAAAGAGAAGT<sup>2</sup>TCC<sup>3</sup>AAGCATGTGTGACAAATCCATGATCAA<sup>4</sup> :  
323  
TrCHS3cs : TG<sup>1</sup>-----ACAAT<sup>2</sup>CCTGAAC<sup>3</sup>TAAACAGAAACT<sup>4</sup>TTGCTAG<sup>5</sup>CACTTTGTAAAGAC<sup>6</sup>AACCAACGGTAA<sup>7</sup> :  
314  
TrCHS3fs : TG<sup>1</sup>-----ACGATACTTATATTAAGGAGAAAT<sup>2</sup>TGGAG<sup>3</sup>CGTCTTTGCAAAAACACA<sup>4</sup>ACTGTGAA<sup>5</sup> :  
330

329  
TrCHShs : CGAACATATGACTGATCTTAAGGAAAAATCAAGCGGATGTCGATAGATCAATGATAAA :  
354

TrCHS3as : GAGCAGATACATGTATCTAACAGAAGAGATTTTGAAAGAAAATCCTAGTCTTTGTCAATA :  
383  
TrCHSs : AACAAGGTATGTTGTTATGAATGAGGAGATACTAAAGAAATATCCAGAATTGTTGTCGA :  
374  
TrCHSfs : AACAAGATACACAGTAATGTCAAAGGAGATCTTAGACAACCTATCCAGAGCTAGCCATAGA :  
389  
TrCHShs : GAAACGTTACATGCACCTAACAGAAGACTTTCTGAAGGAGAATCCAAATATGTGTGAATA :  
414

TrCHS3as : CATGGCACCTTCTATTGGATGCTAGGCAAGACATGCTGGTGCTTGAAGTACCTAGACTTGG :  
443  
TrCHSs : AGGCGCCTCAACTGTAAACAAACGTTTATAGATATGTAATGAGGCAGTAACACAAATGGC :  
434  
TrCHSfs : TGGAAACACCAACATAAGGCCAAAGCTTGAAATAGCAAAATCCAGCAGTAGTTGAAATGGC :  
449  
TrCHShs : CATGGCACCATCTACTAGTGTAAAGAGAGACATAGTGGTTGTTCAAGTACCAAAGCTAGG :  
474

TrCHS3as : GAAGGAGGCTGAGTCAAGGCCATTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCA :  
503  
TrCHSs : AATTGAAGCTTCCCAAGTTTGCCCTAAAGAAATGGGGTAGATCCTTATCGGACATAACTCA :  
494  
TrCHSfs : AACAAGAGCAAGCAAAAGATTGCATCAAAAGAAATGGGGAAGGTCACTCAAGATATCACACA :  
509  
TrCHShs : TAAAGAAGCAGCAAAAAAGCCATATGTCAATGGGGACAACCAAAATCAAAATCACACA :  
534

TrCHS3as : CTTAATCTTTTGCACCAAGTGGTGTGACATGCCTGGTGCTGATTACCAACTCACAAA :  
563  
TrCHSs : TGTGGTTTATGTTTCTCTAGTGAAGCTAGATTACCGGGTGGTGACCTATACTTGTCAAA :  
554  
TrCHSfs : CATAGTCTATGTTTCTCGAGCGAAATTCGTCTACCGGGTGGTGACCTTTATCTTGCAAA :  
569  
TrCHShs : TCTTGTTTTCTGCACCACTTCGGGTGTTGACATGCCGGGAGCCGATTACCAACTCACCAA :  
594

TrCHS3as : ACTCTTAGGTCTTCGCGCATATGTGAAAAGGTATATGATGTACCAACAAGGTTGTTTTCG :  
623  
TrCHSs : AGGACTAGGACTAAACCTTAAATTCAAAGAACCATGCTCTATTCTCTGGATGCTCGGG :  
614  
TrCHSfs : TGAACCTCGGCTTAAACAGCGATGTTAATCGCGTAATGCTCTATTTCCTCGGTTGCTACGG :  
629  
TrCHShs : ACTTTTAGGCTTAAACCTTCTGTCAAGCGTCTCATGATGTATCAACAAGGTTGTTTTCG :  
654

TrCHS3as : AGGAGGACCGGTGCTTCGTTTGGCAAAAGATTTGCCCGAGAACAACAAAGCTGCTCGTGT :  
683  
TrCHSs : AGGCCTAGCCGGCCTTCGCGTTGCGAAAGACGTAGCTGAGAACAACCCCTGAAGTAGAGT :  
674  
TrCHSfs : CGGTCTCACTGGCTTACGTCTCGCCAAAGACATCCCGGAAAATAACCCCTGCTAGTAGGGT :  
689  
TrCHShs : TGGCGGCACAGTTCTCCGCTTAGCAAAAGACCTTCTTGAGAATAACAAAAATGCAAGAGT :  
714

TrCHS3as : GCTAGTTGTTTGTCTGAAGTCACCGCAGTCACATTTCGCGGCCCCAGTGATACTCACTT :

743  
 TrCHScs : TTTGCTTGCCTACCTCGGAAACTACAATTATTGGATTCAAGCCACCAAGTGTGATAGACC :  
 734  
 TrCHSfs : GTTACTCACAAACATCCGAGACCACCTATTCTCGGTTTTCCACCACCGAGTAAAGCTAGACC :  
 749  
 TrCHShs : TCTTGTTCGTTGTTCTGAAATTACTGCCGTTACTTTTCCGTGGACCATCGGATACCTCATCT :  
 774  
  
 TrCHS3as : GGACAGTCTTGTGGACAAGCATTGTGGAGATGGAGCCGCTGCACCTAATTGTTGGTTC :  
 803  
 TrCHScs : TTATGATCTTGTGGTGTGGCACTCTTGGAGATGGTGCTGGTGCATGATAATTGGCTC :  
 794  
 TrCHSfs : TTATGACCTCGTGGCGCTGCACCTTTTCGGTGATGGCGCGCTGCTGCAATAATTGGAAC :  
 809  
 TrCHShs : TGATTCGCTCGTGGACAGCGCTTTTGGTGATGGAGCGCAGCAATGATTATTGGCTGC :  
 834  
  
 TrCHS3as : TGATCCAGTGCCTGAAATTGAGAAACCAATATTGACATCGTTGGACTGCACAAACAAT :  
 863  
 TrCHScs : AGACCCGCTATTGAAACTGAGACACCATTCGTTGAGCTGCACTTCAGCTCAGGAGTT :  
 854  
 TrCHSfs : AGACCTATATTGAATCAAGAATCACCTTTCATGGAATTCAACCATGCAGTCCAAAAATT :  
 869  
 TrCHShs : GCATCCTGATTAACCGTGGACGTCGGATTTCGAGATTGTTCGGCTGCTCAGACTAT :  
 894  
  
 TrCHS3as : TGCTCCAGACAGTGAAGGTGCCATTGATGCTCATCTTCGTGAAGCTGGGCTAACATTTC :  
 923  
 TrCHScs : TATACCAGACACCAGAGAAATAATTGATGGCGGCTGACGGAGGAGGGCATAAGTTTCAC :  
 914  
 TrCHSfs : CTGCGTGATACAAAAATGTGATTGATGGTAGAATCACAGAAGGGTATTAAATTTAA :  
 929  
 TrCHShs : TCTTCCTGATTCTGATGGCGCAATTGATGACATCTTCGTGAAGTGGGCTCACITTTCA :  
 954  
  
 TrCHS3as : TCTTCTTAAGATGTTCCCTGGGATTGTATCAAAGAACATTAA-----TAAAGCATT :  
 974  
 TrCHScs : ACTAGCAAGGGAAC TTCGCAGATAATCGAAGACAATGTTGAGGGATTCTGTAATAAAGT :  
 974  
 TrCHSfs : GCTTGAAGAGACCTTCCTCAAAAAATTGAAGACAATATTGA-----AGAATTTT :  
 979  
 TrCHShs : TTATTGAAAGATGTTCCGGGATTATTTCAAAGAACATTCA-----AAAAAGTTT :  
 1005  
  
 TrCHS3as : GGTTGAGGCTTTCCAACCA-TTAGGAATTTCTGACTACAACCTCAATCTTTTGGATTGCAC :  
 1033  
 TrCHScs : AATTGATCTTGTTCGG-----TTGGAGATAAGGAGTACAATAAGTTGTTTGGGCTGTGC :  
 1030  
 TrCHSfs : GCAAGAAAATTATGGCTAAAAGTGATGTTAAGGAATTTAATGACTTATTTTGGGCTGTT :  
 1039  
 TrCHShs : AGTTGAAGCTTTTCGCCT-ATTGGGATTAATGATTGGAAGTCAATATTTTGGGTTGCAC :  
 1064  
  
 TrCHS3as : ACCGGGTGGACCTGCAATCTTGATCAAGTAGAACAAGCTAGCCCTCAAGCCCCGAAA :  
 1093  
 TrCHScs : ATCCAGGTGGCCCTCGGATATTGAATCGCTGGAGAGCGGCTTGAGTTTCGCCGCAG :  
 1090  
 TrCHSfs : ATCCTGGTGGGCCAGCTATACTCAATAAGCTAGAAAATATACTCAAAATGAAAAGTCATA :  
 1099

TrCHShs : **AATCCAGGTGGACCGGCTATTTTAGACCAAGCTTGAAGAGAACTCCATCTTAAAGAGGACA** :  
 1124  
 TrCHS3as : **AGATCAGGGCCACGAGGGAAGTTCTAACTGAATATGGAAACATGTCAGCGCATGTGTAT** :  
 1153  
 TrCHSs : **AGCTCAATGCTACTAGAAAAGCTCTAATGATTATGGAAA--TGCTAGCAGCAATACTAT** :  
 1148  
 TrCHSfs : **AATTGGATTGTAGTAGCAAGGCATTAAATGATTATGGAAA--TCTTAGTAGCAATACTAT** :  
 1157  
 TrCHShs : **AACTCCGGTCCACCCGCCATGTGCTTAGTGAATATGGAAATATGTCAGTGCATGTGT** :  
 1184  
 TrCHS3as : **TGTTTCATCT--TAGATGAGATCGGAAGAAATCGGCTCAAAATCCACTTAAGACAAC** :  
 1211  
 TrCHSs : **TGTTTATGT--GCTGGAATATATGCTAGAAAG--CGAAAAGAGATTAAAAGGCGGGTGG** :  
 1205  
 TrCHSfs : **ATCTATGTGATGAGTATATGAGAGATTATTCGAAGGAAGATGCAAGTGAAGAATGGG** :  
 1217  
 TrCHShs : **TATTTATTT--TGGATGAATCAGAAAGGCTCTAAGAGGAAGCGATGATTACAC** :  
 1242  
 TrCHS3as : **ACAAGGACTTGATTGGGGTGTGTGTTCEGCTTCGGA-----CC-----AGCACTTA** :  
 1258  
 TrCHSs : **AGGAGATCTGAATGGGATTGATACTTCCTTTTGGG-----CC-----TGCAATTA** :  
 1252  
 TrCHSfs : **ATTAGCATTTGGCTTTTGGACCAGGCATTACTTTTGAAGGGGTTCTCTCCGTAGCCTTA** :  
 1277  
 TrCHShs : **TCAAGGGTTGCAATGGGGTGTGTGTTTGGCTTTGGA-----CC-----GGCTTTAA** :  
 1289  
 TrCHS3as : **CATTGAAACCGTTCTTCTTCGTA-----CCGTCG-----** :  
 1290  
 TrCHSs : **CTTTTGAGGGGATTCTAGCAAGGAAGTTCTGTCATGAAGTCTTATACT-----ATTGTG** :  
 1307  
 TrCHSfs : **ATCTTGAAATAATAATTCATATGAAATTACTTCTCTTAAGATTGTGATGGAAGATGAAT** :  
 1337  
 TrCHShs : **CTGTTGAAACCGTTCTGCTTCATA-----CTGTCCGGTTCAGGTTGAA-----TTTATT** :  
 1340  
 TrCHS3as : **ATATA-----AGATGTG-----** :  
 1302  
 TrCHSs : **ATGCATGACTT--ATCTCTTATT--TCTACTAATTATTATATTAGCAAAATTCAG---** :  
 1359  
 TrCHSfs : **ATGTATTGGATTAAATATGATATGGTGTTATTTTAAGTTGATTTTAAAAAAGTTTATTA** :  
 1397  
 TrCHShs : **ATACATAGATTGGAAATAAAATT--TGCCTGCCGAGACATGTGAACTAACTTTGT---** :  
 1394  
 TrCHS3as : **-----TGA-----TTCT-TTTTA** :  
 1315  
 TrCHSs : **---AACTTTTAAGTAA--TGATTTAATGAAGAATACTTATAGTATATTGA-CTTTATTC** :  
 1412  
 TrCHSfs : **ATAAGTATGATGTAACTTGTGTTTGAATGTAAAAAGGGAAGTATACTAATTTAAGT** :  
 1457  
 TrCHShs : **---AGGCAAGCTCAA--TTAAAGTTTGAG--ATAATATTGTGCTTTAGT-TATTATGG** :  
 1445  
 TrCHS3as : **---TTTAAATGLATTACTTTTAAATCTTGCTCC---C-----TTGAATTTCG--ATT** :

1357  
 TrCHS3as : ACTTTTCAAAGCAACTTTATGATCCTAA-GACATGG-----TACAACTTGGAGCATG :  
 1461  
 TrCHSfs : TCTTGACCATACCTGATTTTTCTTTACACATTTCATATCTAAAAATTGTTCTATCATATC :  
 1517  
 TrCHShs : TATGTAATGTAATCTTTTACTTTTTCGAAATTC-----ATGTAATTTC--ATA :  
 1493  
  
 TrCHS3as : T-----A-AG-AATA-----AATAAATATATCTTT :  
 1380  
 TrCHS3as : TGGT-----ATAGTTGTAACAAAACTCTA-----AGCAAAATAGAGACTT :  
 1501  
 TrCHSfs : TTCATTGTTGATCTGTAATAATATAATACTAATTGGCTGGCAAAATGAAAGATTTTT :  
 1577  
 TrCHShs : TGT-----A-AGTAATATGTTTGGGTGG-----AATATAATTATTTGT :  
 1532  
  
 TrCHS3as : TGA-TAAAAAAAAA-----AAAAAAAAAAAAAAAAAGTACTCTGCGTTGTTACCACTG :  
 1434  
 TrCHS3as : TATGTAGTATAAAGCATTTCCAGACATGATAAATAATGGTAC-CTCAGAACATAAAATAT :  
 1560  
 TrCHSfs : CACCGAAAAAAAAA-----AAAAAAAAAAAAAAAAAGTACTCTGCGTTGTTACCACTG :  
 1634  
 TrCHShs : TAACTAAAAAAAAA-----AAAAAAAAAAAAAAAAAGTACTCTGCGTTGTTACCACTG :  
 1587  
  
 TrCHS3as : CTTAATCGAATTC----- :  
 1447  
 TrCHS3as : ATTTAGCTATCTTTTCATCCCAACTTTACACATCCACCAAGGTACAGAATAAGCATATGT :  
 1620  
 TrCHSfs : CTTAATCACTAGTGAATTC----- :  
 1653  
 TrCHShs : CTTAATCGAATTC----- :  
 1600  
  
 TrCHS3as : ----- :  
 -  
 TrCHS3as : CAACACAAAATGTACTCTAAGTCTAACATGAGTAACCAAACATGATGCCTGATTAAGTTA :  
 1680  
 TrCHSfs : ----- :  
 -  
 TrCHShs : ----- :  
 -  
  
 TrCHS3as : ----- :  
 -  
 TrCHS3as : AAAGAAAAGAAAATCTGAGGGCATAGATCTTCAATCACACCACTCCAGAGGGAAGGCGTA :  
 1740  
 TrCHSfs : ----- :  
 -  
 TrCHShs : ----- :  
 -  
  
 TrCHS3as : ----- :  
 -  
 TrCHS3as : GAACAAGCTGTCCGCCGAAAACACTGCAATTCAATAAATATCATTAGGACAACAGTGCAG :  
 1800  
 TrCHSfs : ----- :  
 -  
 TrCHShs : ----- :

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-
TrCHS3as : ----- :
-
TrCHS3as : AGTCATGCGGGAAATGTCTTAAGTCACTGTACTAAAAATATAGGATTATATTATGAACTA :
1860
TrCHSfs : ----- :
-
TrCHShs : ----- :
-

TrCHS3as : ----- :
-
TrCHS3as : TACTAACCTTTTCACATAATAGTAACAGAAATCAGCTAAGATGAATGTCTGGACAATTTC :
1920
TrCHSfs : ----- :
-
TrCHShs : ----- :
-

TrCHS3as : ----- :
-
TrCHS3as : TGAGATAAGAACCATGACGGCCATAAGCCATACCCCAAGGCAACCAATAAATGTCCACGG :
1980
TrCHSfs : ----- :
-
TrCHShs : ----- :
-

TrCHS3as : ----- :
-
TrCHS3as : GTATCTAACACCTGTTGCAAGAAATAGTAAGTTATTAGGAGATGTGCGGTTACGAAATTC :
2040
TrCHSfs : ----- :
-
TrCHShs : ----- :
-

TrCHS3as : ----- :
-
TrCHS3as : AAGCTACACAACAAAAGGAGGCCAGAACAACAGCAATCTTGTAACCAGATGACAACAATA :
2100
TrCHSfs : ----- :
-
TrCHShs : ----- :
-

TrCHS3as : ----- :
-
TrCHS3as : AAATGTAAACTTAAAGAGACCGAACACACAAACATTGCAACTCAGATGGAATTGCTGCCA :
2160
TrCHSfs : ----- :
-
TrCHShs : ----- :
-

TrCHS3as : ----- :
-

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TrCHS3cs : TGTAAC TAGTAGGAGATTTGGGACGTCAAATCAGTATATTATGCAAAATACAAGGTATGAC :
2220
TrCHS3fs : ----- :
-
TrCHS3hs : ----- :
-

TrCHS3as : ----- :
-
TrCHS3cs : CGCCTTGTCTATTGTAGCATACAACAAACGTACAGTGGGTTTGTCCCTCTCAAATGGCA :
2280
TrCHS3fs : ----- :
-
TrCHS3hs : ----- :
-

TrCHS3as : ----- :
-
TrCHS3cs : GGATCTTTACAGCACAAATATTTGGTTTTGTCATACTTATACCATAAAAAAAAAAAAAAAAA :
2340
TrCHS3fs : ----- :
-
TrCHS3hs : ----- :
-

TrCHS3as : ----- :
TrCHS3cs : AAAAAAAAAAAAAAGTACTCTGCGTTGTTACCACTGCTTAATCACTAGTGAATTC : 2394
TrCHS3fs : ----- :
TrCHS3hs : ----- :

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**TrLAR nucleotide sequence alignment**

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TrLARas : GAATTCGATTAAGCAGTGGTAACAACGCAGAGTACGCGGG-----AT :
43
TrLARbs : GAATTCGATTAAGCAGTGGTAACAACGCAGAGTACGCGGGAGGATCCTTCCATTTTGCAT :
60
TrLARcs : GAATTCGATTAAGCAGTGGTAACAACGCAGAGTACGCGGG-----AT :
43

TrLARas : ACCAACATTGTCACAATTAAGTCTAAAAGCAAAGCAATGGCACCAGCAGCAACATCATCA :
103
TrLARbs : ACCAACATTGTCACAATTAAGTCTAAAAGCAAAGCAATGGCACCAGCAGCAACATCATCA :
120
TrLARcs : ACCAACATTGTCACAATTAAGTCTAAAAGTAAAGCAATGGCACCAGCAGCAACATCATCA :
103

TrLARas : CCAACCACTCCACTACTACCAAGGGTCGTGTCCTAATTGTTGGAGGAACAGGTTTCATT :
163
TrLARbs : CCAACCACTCCACTACTACCAAGGGTCGTGTCCTAATTGTTGGAGGAACAGGTTTCATT :
180
TrLARcs : CCAACCACTCCACTACTACCAAGGGTCGTGTCCTAATTGTTGGAGGAACAGGTTTCATT :
163

TrLARas : GGAAAATTTGTAAGTGAAGGCAAGTCTTTCCACAACACACCCAACCTACTTGTGTTGTTTCGG :
223
TrLARbs : GGAAAATTTGTAAGTGAAGGCAAGTCTTTCCACAACACACCCAACCTACTTGTGTTGTTTCGG :
240
TrLARcs : GGAAAATTTGTAAGTGAAGGCAAGTCTTTCCACAACACACCCAACCTACTTGTGTTGTTTCGG :
223

TrLARas : CCAGGACCTCTTCTCTCTTCTAAGGCTGCCACTATTAAGGCATTCCAAGAGAAAGGTGCC :
283
TrLARbs : CCAGGACCTCTTCTCTCTTCTAAGGCTGCCACTATTAAGGCATTCCAAGAGAAAGGTGCC :
300
TrLARcs : CCAGGACCTCTTCTCTCTTCTAAGGCTGCCACTATTAAGGCATTCCAAGAGAAAGGTGCC :
283

TrLARas : ATTGTCATTTATGGTCGGGTAAATAATAAGGAGTTCATGGAGATGATTTTGAAAAAGTAT :
343
TrLARbs : ATTGTCATTTATGGTCGGGTAAATAATAAGGAGTTCATGGAGATGATTTTGAAAAAGTAT :
360
TrLARcs : ATTGTCATTTATGGTCGGGTAAATAATAAGGAGTTCATGGAGATGATTTTGAAAAAGTAT :
343

TrLARas : GAGATAAATGTAGTCATTTCTGCAATAGGAGGCTCTGATGGCTTGCTGGAACAGCTTACT :
403
TrLARbs : GAGATAAATGTAGTCATTTCTGCAATAGGAGGCTCTGATGGCTTGCTGGAACAGCTTACT :
420
TrLARcs : GAGATAAATGTAGTCATTTCTGCAATAGGAGGCTCTGATGGCTTGCTGGAACAGCTTACT :
403

TrLARas : TTGGTGGAGGCCATGAAATCTATTAACACCATTAAGAGGTTTTTGCCTTCGAATTTGGT :
463
TrLARbs : TTGGTGGAGGCCATGAAATCTATTAACACCATTAAGAGGTTTTTGCCTTCGAATTTGGT :
480
TrLARcs : TTGGTGGAGGCCATGAAATCTATTAACACCATTAAGAGGTTTTTGCCTTCGAATTTGGT :
463

TrLARas : CACGATGTGGACAGAGCAATATCCTGTGGAACCTGGCCTAACAATGTACAAACAGAAACGT :

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523  
 TrLARbs : CACGATGTGGACAGAGCAATCCTGTGGAACCTGGCCTAACAATGTACAAACAGAAACGT :  
 540  
 TrLARcs : CACGATGTGGACAGAGCAATCCTGTGGAACCTGGCCTAACAATGTACAAACAGAAACGT :  
 523  
  
 TrLARas : TTGGTTAGACGTGTGATCGAAGAATCTGGTTACCATACACCTACATCTGTTGCAATTCTG :  
 583  
 TrLARbs : TTGGTTAGACGTGTGATCGAAGAATCTGGTTACCATACACCTACATCTGTTGCAATTCTG :  
 600  
 TrLARcs : TTGGTTAGACGTGTGATCGAAGAATCTGGTTACCATACACCTACATCTGTTGCAATTCTG :  
 583  
  
 TrLARas : ATCGCATCTTGGCCGTACTATGACAATTGTCATCCATCACAGCTTCTCCACCGTTGGAT :  
 643  
 TrLARbs : ATCGCATCTTGGCCGTACTATGACAATTGTCATCCATCACAGCTTCTCCACCGTTGGAT :  
 660  
 TrLARcs : ATCGCATCTTGGCCGTACTATGACAATTGTCATCCATCACAGCTTCTCCACCGTTGGAT :  
 643  
  
 TrLARas : CAATTACATATTTATGGTCATGGCGATGTCAAAGCTTACTTTGTTGATGGCTATGATATT :  
 703  
 TrLARbs : CAATTACATATTTATGGTCATGGCGATGTCAAAGCTTACTTTGTTGATGGCTATGATATT :  
 720  
 TrLARcs : CAATTACATATTTATGGTCATGGCGATGTCAAAGCTTACTTTGTTGATGGCTATGATATT :  
 703  
  
 TrLARas : GGGAAATTCACAATGAAGGTCATTGATGATGAAAGAACAATCAACAAAAATGTTTCATTTT :  
 763  
 TrLARbs : GGGAAATTCACAATGAAGGTCATTGATGATGAAAGAACAATCAACAAAAATGTTTCATTTT :  
 780  
 TrLARcs : GGGAAATTCACAATGAAGGTCATTGATGATGAAAGAACAATCAACAAAAATGTTTCATTTT :  
 763  
  
 TrLARas : CGACCTTCTAACAATTGTTATAGCATGAATGAGCTTGCTTCTTTGTGGGAAAACAAAATT :  
 823  
 TrLARbs : CGACCTTCTAACAATTGTTATAGCATGAATGAGCTTGCTTCTTTGTGGGAAAACAAAATT :  
 840  
 TrLARcs : CGACCTTCTAACAATTGTTATAGCATGAATGAGCTTGCTTCTTTGTGGGAAAACAAAATT :  
 823  
  
 TrLARas : GCACGAAAAATTCCTAGAGTGATCGTCTCTGAAGACGATCTTCTAGCAATAGCCGCAGAA :  
 883  
 TrLARbs : GCACGAAAAATTCCTAGAGTGATCGTCTCTGAAGACGATCTTCTAGCAATAGCCGCAGAA :  
 900  
 TrLARcs : GCACGAAAAATTCCTAGAGTGATCGTCTCTGAAGACGATCTTCTAGCAATAGCCGCAGAA :  
 883  
  
 TrLARas : AATGTCATACCGGAAAGTGTGTGGCAATCACTCATGATATATTCATCAATGGATGT :  
 943  
 TrLARbs : AATGTCATACCGGAAAGTGTGTGGCAATCACTCATGATATATTCATCAATGGATGT :  
 960  
 TrLARcs : AATGTCATACCGGAAAGTGTGTGGCAATCACTCATGATATATTCATCAATGGATGT :  
 943  
  
 TrLARas : CAAGTTAACTTCAAGTAGATGGAATTCATGATGTTGAAATTGGCACTCTATATCCTGGT :  
 1003  
 TrLARbs : CAAGTTAACTTCAAGTAGATGGAATTCATGATGTTGAAATTGGCACTCTATATCCTGGT :  
 1020

TrLARcs : CAAGTTAACTTCAAGATAGATGGAATTCATGATGTTGAAATTGGCACTCTATATCCTGGT :  
 1003

TrLARas : GAATCGGTAAGAAGTTTGGAGGAATGCTATGAGAAATTTGTTGTCATGGCGGCTGACAAG :  
 1063

TrLARbs : GAATCGGTAAGAAGTTTGGAGGAATGCTATGAGAAATTTGTTGTCATGGCGGCTGACAAG :  
 1080

TrLARcs : GAATCGGTAAGAAGTTTGGAGGAATGCTATGAGAAATTTGTTGTCATGGCGGCTGACAAG :  
 1063

TrLARas : ATTCATAAAGAAGAACTGGAGTTACCGCAGGTGGGGGCGGCACAACGGCTATGGTAGAG :  
 1123

TrLARbs : ATTCATAAAGAAGAACTGGAGTTACCGCAGGTGGGGGCGGCACAACGGCTATGGTAGAG :  
 1140

TrLARcs : ATTCATAAAGAAGAACTGGAGTTACCGCAGGTGGGGGCGGCACAACGGCTATGGTAGAG :  
 1123

TrLARas : CCGGTGCCAATCACAGCTTCCTGTTGAAAAGGTTACCTGAGGTGGATATTCTTTTGAGT :  
 1183

TrLARbs : CCGGTGCCAATCACAGCTTCCTGTTGAAAAGGTTACCTGAGGTGGATATTCTTTTGAGT :  
 1200

TrLARcs : CCGGTGCCAATCACAGCTTCCTGTTGAAAAGGTTACCTGAGGTGGATATTCTTTTGAGT :  
 1183

TrLARas : CATAAGACATGTTGATTGTTGATGTTGTTTTCAAGAATGTTTCATCATTTTCATGTGTTTT :  
 1243

TrLARbs : CATAAGACATGTTGATTGTTGATGTTGTTTTCAAGAATGTTTCATCATTTTCATGTGTTTT :  
 1260

TrLARcs : CATAAGACATGTTGATTGTTGATGTTGTTTTCAAGAATGTTTCATCATTTTCATGTGTTTT :  
 1243

TrLARas : ATTAATCCTAAGTACAAATAATTGCTGTCTACGTACGTTCTTAGTTGC AAAAATTCTTGT :  
 1303

TrLARbs : ATTAATCCTAAGTACAAATAATTGCTGTCTACGTACGTTCTTAGTTGC AAAAATTCTTGT :  
 1320

TrLARcs : ATTAATCCTAAGTACAAATAATTGCTGTCTACGTACGTTCTTAGTTGC AAAAATTCTTGT :  
 1303

TrLARas : TATTCTCTATTGAGGTAAAAGTCTTCATGTTTAC----- :  
 1337

TrLARbs : TATTCTCTATTGGGTAAAAGTCTTCATGTTTATTGTTAGTTGTGTTGGTTTTTCATATAT :  
 1380

TrLARcs : TATTCTCTATC----- :  
 1314

TrLARas : ----- :  
 -

TrLARbs : GCTATTTGCAATAATGATTTTTGTGAAGCACTTGTGGTGTATTTACTTACTACTGAAAT :  
 1440

TrLARcs : ----- :  
 -

TrLARas : -----AAAAAAAAAAAAAAAA :  
 1358

TrLARbs : AATGGTTACACAAAATATATAAAAAATAAAAAATAAGCAAAAAAAAAAAAAAAAA :  
 1500

TrLARcs : -----AAAAAAAAAAAAAAAA :  
 1333

TrLARas : AAAAAAAAAAGTACTCTGCGTTGTTACCACTGCTTAATCACTAGTGAATTC : 1409

TrLARbs : AAAAAAAAAAGTACTCTGCGTTGTTACCACTGCTTAATCACTAGTGAATTC : 1551  
TrLARcs : AAAAAAAAAAGTACTCTGCGTTGTTACCACTGCTTAATCACTAGTGAATTC : 1384

## TrCHS amino acid sequence alignment

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TrCHS3ap : MVSVAEIRKAO-----RAEGPATILATGTANPPNRVEQSTYPDFYFKITNSEHKTEL
: 52
TrCHS3cp : MGDEGIVRG-----VTKQTTPGKATILATGKAEPHQLVMOECLVGGYERDTNCDN-PEL
: 53
TrCHS3fp : -MPQGDINGSSSVNGARARRAPTQGKATILATGKAEPHQLVMOECLVEGFIRDTCDD-TYI
: 60
TrCHS3hp : MYTVEEIRNAO-----RSNGPATILATGTATPSNCVTOADYPDYFRITNSEHMTDL
: 52

TrCHS3ap : KEKFORMCDKSMIKSRMYLLEEFILKENPSICEYMAPSLDARQDMVVEVPRLGKEAAVKAI
: 114
TrCHS3cp : KOKLARLCKTTTVKTRYVVMNEEFILKKYPELVVEGASTVKORLETCNEAVTOMAEASQVCL
: 115
TrCHS3fp : KEKLERLCKNTTVKTRYTVMSKEILDNYPELAIDGTFETIROKLEIANPAVVEMATRASKDCI
: 122
TrCHS3hp : KEKEKRMCDRSMIKKRYMHLLEDFILKENPNCYMAPSLDVRDITVVEVVPKLGKEAAKKAI
: 114

TrCHS3ap : KEWGQPKSKITHLIFCTTSGVDMPGADYQLTKLLGLRPPYVKRYMMYQOGCEAGGTIVLRLAKD
: 176
TrCHS3cp : KNWGRSLSDITHVVYVSSSEARLPGGDLYLSKGLGINKIORTMLYFSGCSGGVAGLRVAKD
: 177
TrCHS3fp : KEWGRSPQDITHIVYVSSSEARLPGGDLYLANELGLNSDVNRVMLYELGCGYGGVTGLRVAKD
: 184
TrCHS3hp : CWGQPKSKITHLVFCTTSGVDMPGADYQLTKLLGLKPSVKRLMMYQOGCEAGGTIVLRLAKD
: 176

TrCHS3ap : LAENNKCARVLVVCSEITAVTFRGPSDTHLDSLVGOALFGDGAAAIVGSDPVPLEKPIFE
: 238
TrCHS3cp : VAENNPGRSVLLATSETTITGFKPPSVDRPYDLVGVALFGDGAGAMIIGSDPVFETETPLFE
: 239
TrCHS3fp : LAENNPGRSVLLTTSETTITLGRFPSSKARPYDLVGAALFGDGAAAATIGIDPILNQESPFME
: 246
TrCHS3hp : LVENNKARVLVVCSEITAVTFRGPSDTHLDSLVGOALFGDGAAAAMIIGADEPDITVERPIFE
: 238

TrCHS3ap : MWTAQTIAIPDSEGAIDCHLREAGLIFHLLKDVPGITVSKNINKALVEAFQPLG--ISDYNSI
: 298
TrCHS3cp : LHTSAQEFIPDTEKKIDGRITTEEGISFTLARELPQIIEDNVGFCNKLIDVVGLENKEYNKL
: 301
TrCHS3fp : LNHAVQKFLPDTQNVIDGRITTEEGINFKLGRDLEPKIEDNILEFCKKIMAKS--DVKEFNDI
: 306
TrCHS3hp : IVSAAQTIIIPDSGDAIDCHLREVGLIFHLLKDVPGITISKNIEKSLVEAFAPIG--INDWNSI
: 298

TrCHS3ap : FWIAHPGGPAILDOVEOKLALKPEKMRATREVLSEYGNMSSACVIFILDEMRRKKSANGLKT
: 360
TrCHS3cp : FWAVHPGGPAILNRVEKRIELSPQKINASRKALMDYGNASSNTIFYVLEYMLEEEKKI-KKA
: 362
TrCHS3fp : FWAVHPGGPAILNKLENILKLSDKLDCSRKALMDYGNVSSNTIFYVMEYMDYLYK-----E
: 363
TrCHS3hp : FWVAHPGGPAILDOVEEKHLKEEKLSTRHVLSEYGNMSSACVIFILDEMRRKRSKEEGMIT
: 360

TrCHS3ap : TEGILDWGVLEFGFGPLTITETVVLRSVAI-- : 389
TrCHS3cp : GGDSEWGLILAFGPGITTEGILARNLCA-- : 391
TrCHS3fp : -DGSEWGLGLAFGPGITTEGVLLRSL---- : 389

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TrCHShp : TCEGLEWGVFGFGPGLTIVETVVHSLVVOG : 391

**TrLAR amino acid sequence alignment**

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TrLARap : MAPAATSSPTTPPTTKGRVLIVGGTGFIGKFVTEASLSTTHPTYLLVRPGPLLSSKAATI :
60
TrLARbp : MAPAATSSPTTPPTTKGRVLIVGGTGFIGKFVTEASLSTTHPTYLLVRPGPLLSSKAATI :
60
TrLARcp : MAPAATSSPTTPPTTKGRVLIVGGTGFIGKFVTEASLSTTHPTYLLVRPGPLLSSKAATI :
60

TrLARap : KAFQEKGAIVIIYGRVNNKEFMEMILKKYEINVVISAIGGSDGLLEQLTLVEAMKSINTIK :
120
TrLARbp : KAFQEKGAIVIIYGRVNNKEFMEMILKKYEINVVISAIGGSDGLLEQLTLVEAMKSINTIK :
120
TrLARcp : KAFQEKGAIVIIYGRVNNKEFMEMILKKYEINVVISAIGGSDGLLEQLTLVEAMKSINTIK :
120

TrLARap : RFLPSEFGHDVDRANPVEPGLTMYKQKRLVRRVIEESGIPYTYICCNSIASWPYYDNCHP :
180
TrLARbp : RFLPSEFGHDVDRANPVEPGLTMYKQKRLVRRVIEESGVPYTYICCNSIASWPYYDNCHP :
180
TrLARcp : RFLPSEFGHDVDRADPVEPGLTMYKQKRLVRRVIEESGIPYTYICCNSIASWPYYDNCHP :
180

TrLARap : SQLPPPLDQLHIYGHGDVKAYFVDGYDIGKFTMKVIDDERTINKNVHFRPSNNCYSMNEL :
240
TrLARbp : SQLPPPLDQLHIYGHGDVKAYFVDGYDIGKFTMKVIDDERTINKNVHFRPSNNCYSMNEL :
240
TrLARcp : SQLPPPLDQLHIYGHGDVKAYFVDGYDIGKFTMKVIDDERTINKNVHFRPSNNCYSMNEL :
240

TrLARap : ASLWENKIARKIPRIVSEDDLAIAAENCIPESVVARITHDIFINGCQVNFKIDGIHDV :
300
TrLARbp : ASLWENKIARKIPRIVSEDDLAIAAENCIPESVVASITHDIFINGCQVNFKVDGIHDV :
300
TrLARcp : ASLWENKIARKIPRIVSEDDLAIAAENCIPESVVARITHDIFINGCQVNFKIDGIHDV :
300

TrLARap : EIGTLYPGESVRSLEECYEKFVVMADKIHKEETGVTAGGGGTTAMVEPVPITASC : 356
TrLARbp : EIGTLYPGESVRSLEECYEKFVVMADKIHKEETGVTAGGGGTTAMVEPVPITASC : 356
TrLARcp : EIGTLYPGESVRSLEECYEKFVVMADKIHKEETGVTAGGGGTTAMVEPVPITASC : 356

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